

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 30, 2002, 17:46:11 ; Search time 68.64 Seconds

(without alignments)
521.876 Million cell updates/sec

Title: US-09-357-273a-2

Perfect score: 5139
Sequence: 1 MPARRLLTLFLPLGLGIF.....QPYFHPPEPQPVPYDPAL 977

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

rched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1749.5	34.0	983	Y0G4_CAEEL	Q09499 caenorhabdi
2	1004	19.5	1115	IRE1_YEAST	P32361 saccharomyc
3	295	5.7	971	CI44_CANAL	Q14427 candida alb
4	294	5.7	741	RNSA_HUMAN	Q05823 homo sapien
5	286.5	5.6	659	BYR2_SCHPO	P28829 schizosacch
6	285.5	5.6	647	LIK1_RAT	P33669 rattus norv
7	283.5	5.5	647	LIK1_MOUSE	P33668 mus musculu
8	281.5	5.5	647	LIK1_HUMAN	P33667 homo sapien
9	277.5	5.4	1230	ST20_CANAL	Q92212 candida alb
10	275	5.4	658	PAK1_SCHPO	P50527 schizosacch
11	274	5.3	406	KPBH_RAT	P31335 rattus norv
12	272	5.3	406	KPBH_HUMAN	P15733 homo sapien
13	272	5.3	682	SNK_MOUSE	P33351 mus musculu
14	271.5	5.3	682	SNK_RAT	Q91012 rattus norv
15	269.5	5.2	417	ERK1_CANAL	P28869 candida alb
16	268.5	5.2	499	KCCD_HUMAN	Q13557 homo sapien
17	268.5	5.2	533	KCCD_RAT	P15791 rattus norv
18	266	5.2	679	RNSA_MOUSE	Q05921 mus musculu
19	265	5.2	685	SNK_HUMAN	Q91013 homo sapien
20	262.5	5.1	912	KPCW_HUMAN	Q15139 homo sapien
21	261.5	5.1	733	K6A2_HUMAN	Q15349 homo sapien
22	260.5	5.1	386	KPBG_HUMAN	Q16816 homo sapien
23	260.5	5.1	386	KPBG_RABIT	P00518 onycotylagus
24	259.5	5.0	478	KCCA_MOUSE	P11798 mus musculu
25	259.5	5.0	478	KCCA_RAT	P11775 rattus norv
26	259	5.0	603	PLK1_HUMAN	P33350 homo sapien
27	259	5.0	733	K6AA_XENILA	P10665 xenopus lae
28	258.5	5.0	387	KPBG_RAT	P33286 rattus norv
29	258.5	5.0	740	DKK1_HUMAN	Q15075 homo sapien
30	257.5	5.0	542	CDP3_ORISA	P33664 oryza sativ
31	257.5	5.0	918	KPCW_MOUSE	Q62101 mus musculu
32	257	5.0	542	KCCB_MOUSE	P28652 mus musculu
33	257	5.0	542	KCCB_RAT	P08413 rattus norv

34	257	5.0	664	KCCB_HUMAN	Q1554 homo sapien
35	255.5	5.0	387	KPBG_MOUSE	P07934 mus musculu
36	255.5	5.0	524	PAK2_HUMAN	Q13177 homo sapien
37	255	5.0	532	CDPK_DAUCA	P28582 daucus caro
38	254.5	5.0	752	K6AA_CHICK	P18652 gallus gall
39	254.5	5.0	842	CI4A_YEAST	P48562 saccharomyc
40	254	4.9	415	KCCS_MALDO	Q07250 malus domes
41	254	4.9	805	FUSE_DROME	P23647 drosophila
42	253.5	4.9	603	PLK1_RAT	Q62673 rattus norv
43	252.5	4.9	545	PAK1_MOUSE	Q08643 mus musculu
44	252.5	4.9	603	PLK1_MOUSE	Q07832 mus musculu
45	252.5	4.9	733	K6A2_MOUSE	Q9wut3 mus musculu

ALIGNMENTS

RESULT	ID	Y0G4_CAEEL	STANDARD	PRT	983 AA.
AC	009499				
DT	01-FEB-1996	(Rel. 33, Created)			
DT	01-FEB-1996	(Rel. 33, Last sequence update)			
DT	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	POTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II				
DE	PRECUSOR (EC 2.7.1.-).				
GN	C41C4.4				
OS	Caenorhabditis elegans				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				
OC	Rhabditidae; Pelodierinae; Caenorhabditis				
OX	NCBI_TaxID=6239;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BRISTOL NZ;				
RA	Burton J.;				
RL	Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; Z48045; CA88100.1; -				
DR	HSSP; P00518; IPRK.				
DR	WormPep; C41C4.4; CE01519.				
DR	InterPro; IPR002372; Bac PQO repeat.				
DR	InterPro; IPR000719; Euk PKinase.				
DR	InterPro; IPR002290; Ser_thr_kin_actsite.				
DR	Pfam; PF01011; Bacterial_PQO_2.				
DR	Pfam; PF00069; Pkinase; 1.				
DR	PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.				
DR	PROSITE; PS00108; PROTEIN KINASE ST; 1.				
DR	PROSITE; PS50011; PROTEIN KINASE DOM; 1.				
KW	Hypothetical protein; transferase; Serine/threonine-protein kinase;				
KW	ATP-binding; Transmembrane; Signal.				
FT	CHAIN	1	21	POTENTIAL.	
FT		22	983	POTENTIAL.	
FT				PUTATIVE SERINE/THREONINE-PROTEIN KINASE	
FT				C41C4.4 IN CHROMOSOME II.	
FT	DOMAIN	22	454	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	455	471	POTENTIAL.	
FT	DOMAIN	472	983	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	534	794	PROTEIN KINASE.	
FT	NP BIND	540	548	ATP (BY SIMILARITY).	
FT	BINDING	562	562	ATP (BY SIMILARITY).	
FT	ACT_SITE	652	652	BY SIMILARITY.	
SO	SEQUENCE	983 AA;	111725 MW;	485418434578C0A CRC64;	

Query Match

34.0%; Score 1749.5; DB 1; Length 983;

Best Local Similarity 38.5%; Pred. No. 1.4e-98;
Matches 395; Conservative 167; Mismatches 285; Indels 179; Gaps 26;

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OY 6 LLLLTLLPGIGTSTYLP-----ETLLVSTLDGLHVAVKRT 49
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 LFTFFLL-----FSSVICSTPGFRNDHESIGDEEKTSTIIVSTIDGLRALDST 61
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 50 GIKKTLKEDVLAQPTVHEEP-AFLPDPNDGLTSLKKNNEGLTKLPETPELVQASP 108
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 GEIKTLDEEPLRSPSAVKQGFLLPNLDGLYL--KNSLKLPFNIPQLVHASP 118
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 109 CRSSDGLIYMKKODIMYVIDLTSEK-----QOTLSAFDSCLPST- 151
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 CKNGDILYAGSKDVMFGIDPKGLKVEYLILNIDSKILFLQVEFLTSASADRICPANO 178
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 152 -SLVLTGTETITMYDKTRRELKNNATFYDAAFLPEDEGYKMSHVSNDGLVYVD 210
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 KOTFLGRTREVSMFDEKRNKGTNNATFNDYSAHLLEPVNTWPKHYASSHGILTFD 238
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 211 SESGDVLIQNYASPVYAFYVQREGLRKVMHINAVETLRITFMSGFGRTKMKYPF 270
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 239 RETGMRKEDLKPQVVALYLRLDGLKLPFEVVGKTEMEN--VAKRIEVDQMPYVL 295
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 271 -----PRETEAKSKLPTLYGVKYSTLSYASPSKV-HEGVAVPRGSTPLLEGPQFDG 323
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 296 GVNADPQTSLTNQFPALFVGESSFGLYALDLVHQITVSPKLLGPPLLEGAPAPA 355
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 324 VTIGDKGCV-----ITPSTDKFDPGLSKNKNILNLYNLLIGHETP-LSAST 373
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 356 LTEMKEEYLPKRRPIITNIPSTIKHTSDG-----EYLLGIDHPRPMTNMT 403
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 374 KMLERFPNNLRKRNVPADSEKKSFEVILNVDOTSENAPTYSRDVEEKPAPAPAP 433
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 404 IIPTRYP-----VPGPK-----AIGSTIERPPQLGVE-----PKH 438
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 434 E-----APVDSMKQATITLSTFLIGVAFITTYPLSMHQOQLOHQPO 480
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 439 EDTSFILLNNHPIPFATVTFALLITVMOG-----ROMQOQKST 483
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 481 KELEKIQLOOQOQQLPRHPGDTAODELDTSGVSESSGTSPTSASNSHLSG 540
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 484 SRMDSFEIYNN-----PGE-----SRSAOTSQOS----- 507
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 541 SSASKAGSSPSLEDDDEETSVYIVGKISPCPKDVLGHGAGTIVYRGMDNRDVAVKR 600
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 508 NRGSGMANRKRIEPEG---WMAVSKLWYSPSDILGTGEGTVYVGTGFGREVAVKR 563
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 601 ILPECFSPADREVLRLSEDEHPNVIKFTCEKROFOYIAELCAATLOEYEOCKPAH 660
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 564 VYSEFVKFAHREADLRSDTHPHVIRYECMESDSQFRYLAELCIASLINDYVEQKEVOQ 623
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 661 ---LGLPRTLLQOOTSGLAHLSNIYHRDLKPHNILLSPMNAHGKIKAMSDGLCKK 717
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 624 NVTIALRIT--MKQATDGLAHLSKIVYHRDKMFPONVLTMAKSGEMRAVYISDGLCKR 681
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 718 LAVGRHSFSR--RSGVPTGEMIAPEMLSEDEKENTYVDIFSAGCVYVVSBSGSPF 775
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 682 VQPGNSISRGIASGLACTDGMIAPEVL--ISASTYVDFISLGCIFYVLTSGTGHF 738
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 776 GKSLQROANILLGACSLDCLRPKEHEDYIARELEKMIAMOPKRPASNDYLKHPFESL 835
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 739 GKSLHROANINVGEXTLKL-ADLDDMSLADLLISSMLNVEPLNLTADAVLNHFEFTWS 797
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 836 EKLOLFQDVDSRIEKSLESDGRIYKOLERGGRAVYKMDRENTDPLTDLRKPFYGG 895
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 798 EKRLAFYSDVSDRYEKEDNSPVVARIETDARIYVCGMRETCALCEKPFYTSF 857
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 896 SVRDLLRAMRKKHHYRELPAEVRTELTGLPDPFVCYFTSFPHLLATYPAHELCSHER 955
   | | | | | | | | | | | | | | | | | | | | | | | |
Db 858 SVRDLLRAMRKKHHYRELPAEVRTELTGLPDPFVCYFTSFPHLLATYPAHELCSHER 917
   | | | | | | | | | | | | | | | | | | | | | | | |
OY 956 LFQRY 961
   | | | | | | | | | | | | | | | | | | | | | | | |

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Db 918 VKRY 923

RESULT 2
ID IREL_YEAST STANDARD; PRT; 1115 AA.
AC P32361;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SERINE/THREONINE-PROTEIN KINASE IREL PRECURSOR (EC 2.7.1.-).
GN IREL OR ERN1 OR YHR079C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;

REL (1)
SEQUENCE FROM N.A.
MEDLINE=92326627; PubMed=1625574;
RA NIKAWA J.-I., Yamashita S.;
RT "IREL encodes a putative protein kinase containing a
RT membrane-spanning domain and is required for inositol phototrophy in
RT Saccharomyces cerevisiae."
RL Mol. Microbiol. 6:1441-1446(1992).

REL (2)
SEQUENCE FROM N.A.
MEDLINE=93364990; PubMed=8358794;
RA Mori K., Ma W., Gething M.J., Sambrook J.;
RT "A transmembrane protein with a cdc2+/CDC28-related kinase activity
RT is required for signaling from the ER to the nucleus."
RL Cell 74:743-756(1993).

REL (3)
SEQUENCE FROM N.A.
PC STRAIN=5288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favellio A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kučaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Laretable P., Louis E.J., Macri C., Maris E., Meneses S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).

REL (4)
CHARACTERIZATION.
RX MEDLINE=96272163; PubMed=8670804;
RA Shamu C.E., Walter P.;
RT "Oligomerization and phosphorylation of the Irelp kinase during
RT intracellular signaling from the endoplasmic reticulum to the
RT nucleus."
RL EMBO J. 15:3028-3039(1996).

REL (5)
FUNCTION: DETECTS THE ACCUMULATION OF UNFOLDED PROTEINS. SEEMS TO
BE INVOLVED IN THE UNFOLDED PROTEIN RESPONSE (UPR) PATHWAY BY
INDUCING THE SPLICING OF HAC1.
REL (6)
SUBUNIT: MAY EXIST FIRST AS A MONOMER, AS THE CONCENTRATION OF
UNFOLDED PROTEIN INCREASES. IT PROBABLY OLIGOMERIZES.
REL (7)
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ENDOPLASMIC
RETICULUM.
REL (8)
PTM: AUTOPHOSPHORYLATED MAINLY ON SERINE RESIDUES.
REL (9)
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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or send an email to license@isb-sib.ch).

EMBL; Z11701; CAAT7763.1; -
EMBL; L19640; AAA34489.1; -

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DR EMBL: U10556; AAB68894.1; ALT_INIT.
DR PIR: S22629; S22629.
DR PIR: A47541; A47541.
DR HSSP: P24941; 1A01.
DR SGP: S0001121; IRE1.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
KW Transmembrane; Signal; Transferase; Serine/threonine-protein kinase;
ATP-binding; Glycoprotein; Endoplasmic reticulum; Phosphorylation.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 526 SERINE/THREONINE-PROTEIN KINASE IRE1.
FT DOMAIN 19 526 LUMENAL (POTENTIAL).
FT TRANSNM 527 555 POTENTIAL.
FT DOMAIN 556 1115 CYTOPLASMIC (POTENTIAL).
FT BIND 674 980 PROTEIN KINASE.
FT NP_BIND 680 688 ATP (BY SIMILARITY).
FT BINDING 702 702 ATP (BY SIMILARITY).
FT ACT_SITE 797 797 BY SIMILARITY.
FT MOD_RES 840 840 PHOSPHORYLATION (AUTO-) (PROBABLE).
FT MOD_RES 841 841 PHOSPHORYLATION (AUTO-) (PROBABLE).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 368 368 N->S (IN REF. 1).
FT CONFLICT 625 626 ND->KH (IN REF. 1).
SQ SEQUENCE 1115 AA; 126975 MW; BD65D74E74365945 CRC64;

Query Match 19.5%; Score 1004; DB 1; Length 1115;
Best Local Similarity 27.1%; Pred. No. 2.9e-53;
Matches 305; Conservative 164; Mismatches 328; Indels 330; Gaps 42;

QY 32 LTFVTLDSGLHAVSRKRSIKWTKLED---PVLOY--PTHVE--EPAPLPDPNDGSLYT 84
DB 122 ILIADVEGGLAVDRNRCHITISIEPENFOLIEQPSRLIETETLLIEPFGDNITY 181
QY 85 LGSKNNEGTLKPTIPELVQASPCRSSDGI-----LYMGRKODIWIYVILL 131
DB 182 FNA--HGOLOKRLISIRLOVSTSPHLKTNIVVNDGKIVEDEKYYTGSMTIMYTNML 239
QY 132 TGEKOOTLSSAFD-----SLCPSTILLYGRT--ETTMYDTR 169
DB 240 NGE---IISAFGPGSKNGYFGSGVSDCSPEEKIKLQECENNIVIGKTFELGHSYDGA 295
QY 170 TRELMNATYFPDYAASLPDEDEGDKMSHFVNSGDLVYVDSGDLMIQVYAS--PVYA 228
DB 296 S---YNTY-----STWQAVLVDFPLAL 315
QY 229 FYVWQREGIRKVMHINAVETLRVLFMSGEVG-RITKWKYPPEETAKSKILPTLVYG 287
DB 316 QNTFESKDGK-----CIAFPKDSILASDLDFRIARVSP----- 349
QY 288 KSTSLVYASPMVHGVAVVPRGSLPLLEGQDTGVTG-----DKGECVITPSTD 339
DB 350 -----TFP-----GLIVGLDFVNDLFTFNENILVPH-- 375
QY 340 VKEFDG---LKSKNRLNYLRN---YMLIGHHTPLASATKMLERFPNNLKRHNENYIP 392
DB 376 -PFGNGDHESISKNV-YLDQTSNLSWFLSSONFSLVESAPISRYAS---DRRWYSS 430
QY 393 ADSEKKSFEVY-----NLVDQTSNAPPTVVSADVEEKAHAPAREPAVD----- 438
DB 431 IFEDETLFENALMGVHOIYNNNEYDHLIYENYEKTSNLDITNHK--YPLMLDSSVDITDLHQ 488
QY 439 -----SMLKRMATIIISTFLIGWAFITVPLSMHQOQLOHQPOKEL-EKIO----- 487
DB 489 NNEANSLSKYSM-----PEDLEAYRKRIKIHQISRELDKRNQNSLLIK 530

QY 488 -----LLOQOQOOLPFHPHPPGDTADGELDLTSGPYSESSGTS 524
DB 531 FGSIVYRIETGVFLFLFLICALLQRFKILPPLVYL--LSKIGFPEKEIPIVESKSLN 588
QY 525 SPSTSPRASN-HSLCSGSSASKAGS-----SPSLQD---DQDEETSVYIV----- 566
DB 589 CPSSSENVYTKPDMKSGKGVVEGAVNDSGLKSEKNDNDADDDKSLDLTTEKKRRKG 648
QY 567 -----GKISPCP-----KDVIGHGAEGITVYRGFMDNDRVAKRILPEC 605
DB 649 SSGCKKRRKSRILANIPNEQSLKMLVSEKILGYSGSVWFQSGFQGRPAVAKMLIDF 708
QY 606 FEFADREVOLRESDEHPNVIRYFCTEKDRPOVYALIELCAATLQEYQOKFAHLGLE- 664
DB 709 CIALMEIKLLNEDSDHPVIRYCYSETDRFLYALIELCNLQDLYESKAVNSDENLKL 768
QY 665 -PITLQOFTSGLAHSLNIVHRDLKRNHLLIS-----MPNAHKITAMISD 711
DB 769 QKEYNPISLRQIASGVANLHSLKILHRDLKPNQNLIVSTSRFTADQGTGAENRLILSD 828
QY 712 FGLCKLAVGRHSFSSRGVP--GTGSIAPEMLSH----- 746
DB 829 FGLCKKLDGSSQSFRTNLPNPSGTSGWRAPDELLESNNIQCQETEHESSRHTVYSSDSF 888
QY 747 ---CKENFTYVDIFSAQCVFYVYVSESGSHPGKSLQROANILGACSLD---CLHPK 799
DB 889 YDPFTKRLTRISIDIFSQCQVFIYLSKKNHPGDKYSRESNIRIFSLDEMKCH-DR 947
QY 800 HEDVITARELIEKMIAMPQKRPSSANDVLEKHPFWSLEKOLQFQVDSRIEKESLDGP-- 857
DB 948 SLIAETDLISQIMIDHDLKPLTKAMVLRHPLFWPKSKLFEELKVSDDLTEIENRPPSA 1007
QY 858 IYKOLENGRAVYVKM--DMENITDPLQDTLRKFRYTKGGSVDDLKRAMKKHHRELA 916
DB 1008 LMKFAGSDGFYIPSGDWKVPKDKTFMDNLERKRYHSSKIMDLKALNKHHHEMDPE 1067
QY 917 EYRETLGLPDDFVCFYTSRPHLAHTYRAM-ELCSHRELPQYVF 962
DB 1068 DIAELMGVPDGFYDFTKRPNLLIGVMIYKENISDQILREFLY 1114

RESULT 3
ID CL44_CANAL STANDARD; PRT; 971 AA.
AC 014427:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SERINE/THREONINE-PROTEIN KINASE CL44 (EC 2.7.1.-).
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mtosporic Saccharomycetales; Candida.
OX NCBI_TaxId=5476;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97411146; PubMed=9259554;
RA Leberer E., Ziegelbauer K., Schmidt A., Marcus D., Dignard D., Ash J.,
Johnson L., Thomas D.Y.;
RT "Virulence and hyphal formation of Candida albicans require the
ste20p-like protein kinase Cdc44p."
RT Curr. Biol. 7:539-546 (1997).
CC -!- FUNCTION: ESSENTIAL FOR VIRULENCE AND MORPHOLOGICAL SWITCHING
(HYPHAL FORMATION) OF C. ALBICANS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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